Amendments to the Claims

The listing of claims will replace all prior versions and listings of claims in the application.

Claims 1-13 (Canceled)

14. (Currently Amended) A method of cloning a nucleic acid molecule or a population of nucleic acid molecules comprising:

inserting one or more integration sequences comprising at least one recombination site into at least one nucleic acid molecule to produce one or more integration sequence-containing nucleic acid molecules; and

transferring said one or more integration sequence-containing nucleic acid molecules comprising at least one recombination site into one or more vectors in the presence of one or more recombination protein.

15. (Previously Presented) The method of claim 14, wherein said at least one nucleic acid molecule is genomic DNA, chromosomal DNA or cDNA.

16. (Previously Presented) A method for producing a nucleic acid molecule or a population of nucleic acid molecules comprising:

inserting one or more integration sequences, said one or more integration sequences comprising at least one recombination site, into at least one nucleic acid molecule thereby producing an integration-sequence-containing nucleic acid molecule comprising at least first and second recombination sites; and

causing said at least first and second recombination sites to recombine in the presence of at least one recombination protein.

17. (Original) The method of claim 16, wherein said recombination of said first and second recombination sites results in a circular molecule.

18. (Previously Presented) The method of claim 16, wherein said first and second recombination sites are separated by at least a portion of said integration-sequence-containing nucleic acid molecule.

19. (Original) The method of claim 16, wherein said integration sequence comprises at least one element selected from the group consisting of one or more primer sites, one or more transcription or translation signals or regulatory sequences, one or more termination signals, one or more origins of replication, one or more selectable markers, and one or more genes or portions of genes.

20. (Original) The method of claim 16, wherein said integration sequence comprises one or more origins of replication and/or one or more selectable markers.

Claims 21-26 (Canceled).

27. (Previously Presented) The method of claim 16, wherein said nucleic acid molecule is genomic DNA, chromosomal DNA or cDNA.

Claims 28-31 (Canceled).

32. (Previously Presented) The method of claim 14, wherein said at least one recombination site is a site-specific recombination site.

33. (Previously Presented) The method of claim 16, wherein said first and second recombination sites are site-specific recombination sites.

34. (Previously Presented) The method of any one of claims 32 and 33, wherein said site-specific recombination sites are selected from the group consisting of *lox*P, *att*B, *att*P, *att*L, *att*R, FRT, a recombination site recognized by a resolvase, a bacterial transposable element, an integrating virus, an IS element, a P element of *Drosophila*, a bacterial virulence factor and a mobile genetic element for a eukaryotic organism, or mutants or derivatives thereof.

35. (Previously Presented) The method of any one of claims 32 and 33, wherein said site-specific recombination sites are selected from the group consisting of *lox*P, *att*B, *att*P, *att*L, *att*R, FRT, a recombination site recognized by a resolvase, a bacterial transposable element, an integrating virus, an IS element, a P element of *Drosophila*, a bacterial virulence factor and a mobile genetic element for a eukaryotic organism.

36. (Previously Presented) The method of any one of claims 32 and 33, wherein at least one of said first and said second recombination sites is an *att* site or a mutant or derivative thereof.

37. (Previously Presented) The method of any one of claims 32 and 33, wherein at least one of said first and said second recombination sites is an *att* site.

38. (Previously Presented) The method of claim 36, wherein said *att* site is selected from the group consisting of *att*B, *att*P, *att*L and *att*R, or a mutant or derivative thereof.

39. (Previously Presented) The method of claim 37, wherein said *att* site is selected from the group consisting of *att*B, *att*P, *att*L and *att*R.

40. (Withdrawn) The method of any one of claims 30-33, wherein at least one of said first and said second recombination sites is a *lox* site or a mutant or derivative thereof.

41. (Withdrawn) The method of any one of claims 30-33, wherein at least one of said first and said second recombination sites is a *lox* site.

42. (Withdrawn) The method of claim 40, wherein said *lox* site is a *lox*P site or a mutant or derivative thereof.

43. (Withdrawn) The method of claim 41, wherein said *lox* site is a *lox*P site.

44. (Previously Presented) A method of producing a nucleic acid molecule or a population of nucleic acid molecules, comprising:

(a) obtaining a first nucleic acid molecule comprising at least a first segment which comprises at least first and second recombination sites, wherein said segment comprises at least one integration sequence;

(b) forming a mixture by mixing said first nucleic acid molecule with at least one second nucleic acid molecule comprising at least third and fourth recombination sites in the presence of at least one recombination protein; and

(c) incubating said mixture under conditions favoring recombination at least between said first and third recombination sites and at least between said second and fourth recombination sites, thereby transferring said first segment from said first nucleic acid molecule to said second nucleic acid molecule.

45. (Previously Presented) The method of claim 44, wherein said first segment is flanked on one side by said first recombination site and is flanked on the other side by said second recombination site.

46. (Previously Presented) The method of claim 44, wherein said first, second, third and fourth recombination sites are site-specific recombination sites.

47. (Previously Presented) The method of claim 44, wherein said first, second, third and fourth recombination sites are selected from the group consisting of *lox*P, *att*B, *att*P, *att*L, *att*R, FRT, a recombination site recognized by a resolvase, a bacterial transposable element, an integrating virus, an IS element, a P element of *Drosophila*, a bacterial virulence factor and a mobile genetic element for a eukaryotic organism.

48. (Previously Presented) The method of claim 44 or claim 45, wherein at least one of said first, second, third and fourth recombination sites is an *att* site or a mutant or derivative thereof.

49. (Previously Presented) The method of claim 44 or claim 45, wherein at least one of said first, second, third and fourth recombination sites is an *att* site.

50. (Previously Presented) The method of claim 48, wherein said *att* site is selected from the group consisting of *att*B, *att*P, *att*L and *att*R, or a mutant or derivative thereof.

51. (Previously Presented) The method of claim 49, wherein said *att* site is selected from the group consisting of *att*B, *att*P, *att*L and *att*R.

52. (Withdrawn) The method of claim 44 or claim 45, wherein at least one of said recombination sites is a *lox* site or a mutant or derivative thereof.

53. (Withdrawn) The method of claim 51, wherein at least one of said recombination sites is a *lox* site.

54. (Withdrawn) The method of claim 52, wherein said *lox* site is a *lox*P site or a mutant or derivative thereof.

55. (Withdrawn) The method of claim 53, wherein said *lox* site is a *lox* P site.

56. (Currently Amended) The method of claim 44, further comprising: (d) selecting for ~~said~~ the second nucleic acid molecule of (c), wherein said second nucleic acid molecule of (c) comprises said transferred first segment.

57. (Previously Presented) The method of claim 44, wherein said recombination takes place *in vitro*.